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SEQUENCE LISTING

<110> Hauptmann, Rudolph  
Himmler, Adolph  
Maurer-Fogy, Ingrid  
Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for  
Them

<130> 98,385-J

<140> 09/899,429

<141> 2001-07-03

<150> 09/792,356

<151> 2000-02-23

<150> 08/477,639

<151> 1955-06-07

<150> 08/383,676

<151> 1995-02-01

<150> 08/153,287

<151> 1993-11-17

<150> 07/821,750

<151> 1992-01-02

<150> 07/511,430

<151> 1990-04-20

<160> 87

<170> PatentIn Ver. 2.0

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<222> (1)..(87)

<220>

<221> misc\_feature

<222> (88)..(120)

<223> Portion of TNF-BP pro protein cleaved by  
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<220>

<221> misc\_feature

<222> (606)..(633)

<223> Portion of TNF-BP pro protein cleaved by extracellular proteases following secretion.

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gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96  
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
20 25 30

cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa 144  
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
35 40 45

tat atc cac cct caa aat aat tgc att tgc tgt acc aag tgc cac aaa 192  
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60

gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac 240  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
65 70 75 80

tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc 288  
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95

aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg 336  
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110

gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg 384  
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125

aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc 432  
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140

aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag 480  
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160

aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa 528  
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175

aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg 576  
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190

aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca 624  
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
195 200 205

ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt 672  
 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 210 215 220

tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag 720  
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 225 230 235 240

tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag 768  
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
 245 250 255

ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc 816  
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
 260 265 270

ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg 864  
 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
 275 280 285

ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912  
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
 290 295 300

ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg 960  
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
 305 310 315 320

gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008  
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
 325 330 335

ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac 1056  
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
 340 345 350

act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104  
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
 355 360 365

ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag 1152  
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
 370 375 380

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 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
 385 390 395 400

tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248  
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
 405 410 415

acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296  
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
 420 425 430

tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg 1344  
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
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 <212> PRT  
 <213> Homo sapiens

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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro  
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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
 35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
370 375 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
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Pro Ala Pro Ser Leu Leu Arg  
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 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96  
 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys  
 20 25 30  
 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144  
 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
 35 40 45  
 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192  
 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
 50 55 60  
 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240  
 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
 65 70 75 80  
 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288  
 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
 85 90 95  
 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336  
 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
 100 105 110  
 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384  
 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
 115 120 125  
 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432  
 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
 130 135 140  
 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480  
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 Asn

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 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
 35 40 45

Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
50 55 60  
Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
65 70 75 80  
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
85 90 95  
Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
100 105 110  
Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
115 120 125  
His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
130 135 140  
Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu  
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gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga 87  
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
20 25

<210> 6  
<211> 29  
<212> PRT  
<213> Homo sapiens

<400> 6  
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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly  
20 25



<210> 7  
<211> 33  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)..(33)

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1 5 10

33

<210> 8  
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<212> PRT  
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Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg  
1 5 10

<210> 9  
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<212> DNA  
<213> Homo sapiens

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30

<210> 10  
<211> 10  
<212> PRT  
<213> Homo sapiens

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<210> 11  
<211> 1334  
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<222> (213)..(1325)

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ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180

aatgggagag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233  
Met Gly Leu Ser Thr Val Pro  
1 5

gac ctg ctg ctg cca ctg ggc ctc ctg gag ctg ttg gtg gga ata tac 281  
Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr  
10 15 20

ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329  
Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys  
25 30 35

aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377  
Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn  
40 45 50 55

tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425  
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
60 65 70

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473  
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
75 80 85

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521  
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
90 95 100

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 569  
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
105 110 115

gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 617  
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
120 125 130 135

tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat 665  
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn  
140 145 150

ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc 713  
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr  
155 160 165

tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt	761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	
170 175 180	
aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att	809
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	
185 190 195	
gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc	857
Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro	
200 205 210 215	
ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt	905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly	
220 225 230	
tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt	953
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val	
235 240 245	
tgt ggg aaa tcg aca cct gaa aaa gag ggg gag ctt gaa gga act act	1001
Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr	
250 255 260	
act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc	1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe	
265 270 275	
acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc	1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser	
280 285 290 295	
agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc	1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg	
300 305 310	
aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca	1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr	
315 320 325	
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac	1241
Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp	
330 335 340	
agc gcc cac aag cca cag agc cta gac act gat gac ccc gcg acg ctg	1289
Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu	
345 350 355	
tac gcc gtg gtg gag aac gtg ccc ccg ttg cgc tgg aaggaattc	1334
Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp	
360 365 370	

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<213> Artificial Sequence

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His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys  
35 40 45  
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
50 55 60  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp  
65 70 75 80  
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu  
85 90 95  
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val  
100 105 110  
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg  
115 120 125  
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe  
130 135 140  
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu  
145 150 155 160  
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu  
165 170 175  
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr  
180 185 190  
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser  
195 200 205  
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
210 215 220  
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
225 230 235 240  
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
245 250 255  
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
275 280 285

Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	Pro	Tyr	Gln	Gly
305					310					315					320

Pro	Leu	Gln	Lys	Trp	Glu	Asp	Ser	Ala	His	Lys	Pro	Gln	Ser	Leu	Asp
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Leu Arg Trp  
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<222> (4157)
<223> "n" can be a, g, c, or t
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<221> unsure
<222> (6255)
<223> "n" can be a, g, c, or t
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ctggcattat gccagtaga tgacctatg ggactttcct actnggcagt acatctacgt 360  
attagtcac gctattacca tggatgacg gttttggcag tacatcaatg ggcgtggata 420  
gcggtttgac tcacgggat ttccaagtct ccacccatt gacgtcaatg ggagtttgtt 480  
ttggcaccaa aatcaatggg actttccaaa atgtcgtaac aactccgcc cattgacgca 540  
aatgggcggg aggcgtgtac ggtgggaggt ctatataagc agagctctct ggctaactag 600  
agaaccact gcttaactgg cttatcgaaa ttaatacgac tcaactatagg gagaccaag 660  
cttctgcagg tcgacatcga tggatccgg acctcgagcg cgaattctct agaggatctt 720  
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tggtttgtga ttttagattc caacctatgg aactgatgaa tgggagcagt ggtggaatgc 900  
ctttaatgag gaaaacctgt tttgctcaga agaatgcc tctagtgtg atgaggctac 960  
tgctgactct caacattcta ctctccaaa aaagaagaga aaggtagaag accccaagga 1020  
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ttgctttgct atttacacca caaaggaaaa agctgcactg ctatacaaga aaattatgga 1140  
aaaatatttg atgtatagtg ccttgactag agatcataat cagccatacc acatttgtag 1200  
aggttttact tgctttaaaa aacctccac acctccccct gaacctgaaa cataaaatga 1260  
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<210> 14

<211> 2173

<212> DNA

<213> Artificial Sequence

<220>

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<222> (245)..(1630)

<220>

<223> Description of Artificial Sequence: raTNF-R8

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 ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg ctg tca ctg gtg ctc 289  
 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu  
 1 5 10 15  
 ctg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt 337  
 Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val  
 20 25 30  
 cct tct ctt ggt gac cgg gag aag agg gat aat ttg tgt ccc cag gga 385  
 Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly  
 35 40 45  
 aag tat gcc cat cca aag aat aat tcc atc tgc tgc acc aag tgc cac 433  
 Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His  
 50 55 60  
 aaa gga acc tac ttg gtg agt gac tgt cca agc cca ggg cag gaa aca 481  
 Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr  
 65 70 75  
 gtc tgc gag ctc tct cat aaa ggc acc ttt aca gct tcg cag aac cac 529  
 Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His  
 80 85 90 95  
 gtc aga cag tgt ctc agt tgc aag aca tgt cgg aaa gaa atg ttc cag 577  
 Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln  
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 gtg gag att tct cct tgc aaa gct gac atg gac acc gtg tgt ggc tgc 625  
 Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys  
 115 120 125  
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 Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys  
 130 135 140  
 gtg gac tgc agc ccc tgc ttc aat ggc acc gtg aca atc ccc tgt aag 721  
 Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys  
 145 150 155  
 gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc 769  
 Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser  
 160 165 170 175  
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 Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys  
 180 185 190  
 atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac 865  
 Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp  
 195 200 205  
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agg	ccc	agg	gtc	tac	tcc	atc	att	tgt	agg	gat	tca	gct	cct	gtc	aaa	1009		
Arg	Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys			
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gag	gtg	gag	ggg	gaa	gga	att	gtt	act	aag	ccc	cta	act	cca	gcc	tct	1057		
Glu	Val	Glu	Gly	Glu	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala	Ser			
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Ile	Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe			
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agc	acc	acc	cca	cgc	ttc	agt	cat	cct	gtc	tcc	agt	acc	ccc	atc	agc	1153		
Ser	Thr	Thr	Pro	Arg	Phe	Ser	His	Pro	Val	Ser	Ser	Thr	Pro	Ile	Ser			
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ccc	gtc	ttc	ggg	cct	agt	aac	tgg	cac	aac	ttc	gtg	cca	cct	gta	aga	1201		
Pro	Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val	Pro	Pro	Val	Arg			
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gag	gtg	gtc	cca	acc	cag	ggg	gct	gac	cct	ctc	ctc	tac	gga	tcc	ctc	1249		
Glu	Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu			
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aac	cct	gtg	cca	atc	ccc	gcc	cct	gtt	cgg	aaa	tgg	gaa	gac	gtc	gtc	1297		
Asn	Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val			
			340						345			350						
gcg	gcc	cag	cca	caa	cgg	ctt	gac	act	gca	gac	cct	gcg	atg	ctg	tat	1345		
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			355			360						365						
gct	gtg	gtg	gat	ggc	gtg	cct	ccg	aca	cgc	tgg	aag	gag	ttc	atg	cgg	1393		
Ala	Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg			
370						375						380						
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385						390				395								
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Gly	Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg			
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ctt	tgc	gac	atg	aac	ctg	cgt	ggc	tgc	ctg	gag	aac	atc	cgc	gag	act	1585		
Leu	Cys	Asp	Met	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr			
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 450 455 460

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 <211> 461  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: raTNF-R8

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 Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys  
 35 40 45  
 Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
 50 55 60  
 Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val  
 65 70 75 80  
 Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val  
 85 90 95  
 Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val  
 100 105 110  
 Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys Lys

115					120					125					
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Asp	Cys	Ser	Pro	Cys	Phe	Asn	Gly	Thr	Val	Thr	Ile	Pro	Cys	Lys	Glu
145					150					155					160
Lys	Gln	Asn	Thr	Val	Cys	Asn	Cys	His	Ala	Gly	Phe	Phe	Leu	Ser	Gly
				165					170					175	
Asn	Glu	Cys	Thr	Pro	Cys	Ser	His	Cys	Lys	Lys	Asn	Gln	Glu	Cys	Met
			180					185					190		
Lys	Leu	Cys	Leu	Pro	Pro	Val	Ala	Asn	Val	Thr	Asn	Pro	Gln	Asp	Ser
	195						200					205			
Gly	Thr	Ala	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Leu	Gly	Leu	Cys	Leu
210						215					220				
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225					230					235					240
Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys	Glu
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			260					265					270		
Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu	Gly	Phe	Ser
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305					310					315					320
Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu	Leu	Tyr	Gly	Ser	Leu	Asn
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Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg	Lys	Trp	Glu	Asp	Val	Val	Ala
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	355						360					365			
Val	Val	Asp	Gly	Val	Pro	Pro	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg	Leu
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385					390					395					400
Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg	Arg
				405					410					415	
Arg	Thr	Pro	Arg	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val	Leu

420 425 430

Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu

435 440 445

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<210> 16
<211> 2141
<212> DNA
<213> Artificial Sequence
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<220>  
<221> CDS  
<222> (213)..(1580)
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<223> Description of Artificial Sequence: human TNF-R in
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gac		ctg		ctg		ctg		cca		ctg		gtg		ctc		ctg		gag		ctg		ttg		gtg		gga		ata		tac		281	
Asp		Leu		Leu		Leu		Pro		Leu		Val		Leu		Glu		Leu		Leu		Val		Val		Gly		Ile		Tyr			
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Pro		Ser		Gly		Val		Ile		Gly		Leu		Val		Pro		His		Leu		Gly		Asp		Arg		Glu		Lys			
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Arg		Asp		Ser		Val		Cys		Pro		Gln		Gly		Lys		Tyr		Ile		His		Pro		Gln		Asn		Asn			
		40						45								50												55					
tcg		att		tgc		tgt		acc		aag		tgc		cac		aaa		gga		acc		tac		ttg		tac		aat		gac		425	
Ser		Ile		Cys		Cys		Thr		Lys		Cys		His		Lys		Gly		Thr		Tyr		Leu		Tyr		Asn		Asp			
						60										65										70							
tgt		cca		ggc		ccg		ggg		cag		gat		acg		gac		tgc		agg		gag		tgt		gag		agc		ggc		473	
Cys		Pro		Gly		Pro		Gly		Gln		Asp		Thr		Asp		Cys		Arg		Glu		Cys		Glu		Ser		Gly			
				75								80												85									
tcc		ttc		acc		gct		tca		gaa		aac		cac		ctc		aga		cac		tgc		ctc		agc		tgc		tcc		521	
Ser		Phe		Thr		Ala		Ser		Glu		Asn		His		Leu		Arg		His		Cys		Leu		Ser		Cys		Ser			
		90										95										100											

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg	569
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	
105 110 115	
gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat	617
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	
120 125 130 135	
tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat	665
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	
140 145 150	
ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc	713
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	
155 160 165	
tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt	761
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	
170 175 180	
aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att	809
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile	
185 190 195	
gag aat gtt aag ggc act gag gac tca ggc acc aca gtg ctg ttg ccc	857
Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro	
200 205 210 215	
ctg gtc att ttc ttt ggt ctt tgc ctt tta tcc ctc ctc ttc att ggt	905
Leu Val Ile Phe Phe Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly	
220 225 230	
tta atg tat cgc tac caa cgg tgg aag tcc aag ctc tac tcc att gtt	953
Leu Met Tyr Arg Tyr Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val	
235 240 245	
tgt ggg aaa tcg aca cct gaa aaa gag ggg gag ctt gaa gga act act	1001
Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr	
250 255 260	
act aag ccc ctg gcc cca aac cca agc ttc agt ccc act cca ggc ttc	1049
Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe	
265 270 275	
acc ccc acc ctg ggc ttc agt ccc gtg ccc agt tcc acc ttc acc tcc	1097
Thr Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser	
280 285 290 295	
agc tcc acc tat acc ccc ggt gac tgt ccc aac ttt gcg gct ccc cgc	1145
Ser Ser Thr Tyr Thr Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg	
300 305 310	
aga gag gtg gca cca ccc tat cag ggg gct gac ccc atc ctt gcg aca	1193
Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr	
315 320 325	
gcc ctc gcc tcc gac ccc atc ccc aac ccc ctt cag aag tgg gag gac	1241

Ala	Leu	Ala	Ser	Asp	Pro	Ile	Pro	Asn	Pro	Leu	Gln	Lys	Trp	Glu	Asp		
		330					335					340					
agc	gcc	cac	aag	cca	cag	agc	cta	gac	act	gat	gac	ccc	gcg	acg	ctg	1289	
Ser	Ala	His	Lys	Pro	Gln	Ser	Leu	Asp	Thr	Asp	Asp	Pro	Ala	Thr	Leu		
		345				350					355						
tac	gcc	gtg	gtg	gag	aac	gtg	ccc	ccg	ttg	cgc	tgg	aag	gaa	ttc	gtg	1337	
Tyr	Ala	Val	Val	Glu	Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val		
		360			365				370					375			
cgg	cgc	cta	ggg	ctg	agc	gac	cac	gag	atc	gat	cgg	ctg	gag	ctg	cag	1385	
Arg	Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln		
			380					385						390			
aac	ggg	cgc	tgc	ctg	cgc	gag	gcg	caa	tac	agc	atg	ctg	gcg	acc	tgg	1433	
Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr	Trp		
			395				400						405				
agg	cgg	cgc	acg	ccg	cgg	cgc	gag	gcc	acg	ctg	gag	ctg	ctg	gga	cgc	1481	
Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu	Gly	Arg		
		410					415				420						
gtg	ctc	cgc	gac	atg	gac	ctg	ctg	ggc	tgc	ctg	gag	gac	atc	gag	gag	1529	
Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp	Ile	Glu	Glu		
		425				430				435							
gcg	ctt	tgc	ggc	ccc	gcc	gcc	ctc	ccg	ccc	gcg	ccc	agt	ctt	ctc	aga	1577	
Ala	Leu	Cys	Gly	Pro	Ala	Ala	Leu	Pro	Pro	Ala	Pro	Ser	Leu	Leu	Arg		
		440			445				450				455				
tga	ggctgcgccc	ctgcgggcag	ctctaaggac	cgctcctgcga	gatcgccttc											1630	
caaccccact	tttttctgga	aaggaggggt	cctgcagggg	caagcaggag	ctagcagccg											1690	
cctaacttgg	gctaaccct	cgatgtacat	agcttttctc	agctgcctgc	gcgccgccga											1750	
cagtcagcgc	tgtgcgcgcg	gagagaggtg	cgccgtgggc	tcaagagcct	gagtgggtgg											1810	
tttgcgagga	tgagggacgc	tatgcctcat	gcccgttttg	ggtgtcctca	ccagcaaggc											1870	
tgtcggggg	cccctgggtc	gtccctgagc	ctttttcaca	gtgcataagc	agtttttttt											1930	
gtttttgttt	tgttttgttt	tgtttttaaa	tcaatcatgt	tacactaata	gaaacttggc											1990	
actcctgtgc	cctctgcctg	gacaagcaca	tagcaagctg	aactgtccta	aggcaggggc											2050	
gagcacggaa	caatggggcc	ttcagctgga	gctgtggact	tttgtacata	cactaaaatt											2110	
ctgaagttaa	aaaaaaaaaa	aaaaggaatt	c													2141	

<210> 17

<211> 455

<212> PRT

<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: human TNF-R in  
1TNF-R2

<400> 17

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1				5				10						15		
Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	Val	Pro	
			20					25					30			
His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	
		35					40					45				
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	
	50					55					60					
Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	
	65				70					75					80	
Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	
				85					90					95		
Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	
			100					105					110			
Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	
		115					120					125				
Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	
	130					135					140					
Asn	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	
	145				150					155					160	
Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	
				165					170					175		
Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr	
			180					185					190			
Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser	
		195					200					205				
Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu	
	210					215					220					
Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys	
	225				230					235					240	
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu	
				245					250					255		
Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser	
			260					265					270			

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val  
           275                                  280                                  285  
 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys  
           290                                  295                                  300  
 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly  
 305                                  310                                  315                                  320  
 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn  
                                   325                                  330                                  335  
 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp  
                                   340                                  345                                  350  
 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro  
           355                                  360                                  365  
 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu  
           370                                  375                                  380  
 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln  
 385                                  390                                  395                                  400  
 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala  
                                   405                                  410                                  415  
 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly  
                                   420                                  425                                  430  
 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro  
           435                                  440                                  445  
 Pro Ala Pro Ser Leu Leu Arg  
           450                                  455

<210> 18  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: N-terminal  
           amino acid sequence of protein purified from urine  
           (main sequence)

<220>  
 <221> UNSURE  
 <222> (4)  
 <223> Identity of "Xaa" could not be determined.

<400> 18  
 Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln  
   1                                  5                                  10

<210> 19  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: N-terminal  
amino acid sequence of protein purified from urine  
(sudsidiary sequence)

<220>  
<221> UNSURE  
<222> (7)  
<223> Identity of "Xaa" could not be determined.

<400> 19  
Leu Val Pro His Leu Gly Xaa Arg Glu  
1 5

<210> 20  
<211> 151  
<212> DNA  
<213> Homo sapiens

<400> 20  
caggggaaaa tattcaccct caaataattc gatttgctgt accaagtgcc acaaaggaaa 60  
ctacttgtag aatgactgtc caggcccggg gcaggatagc gactgcaggg agtgtgagag 120  
cggctccttc acagcctcag aaaacaacaa g 151

<210> 21  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 21  
Asp Ser Val Cys Pro Gln Gly Lys  
1 5

<210> 22  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>

<221> UNSURE  
 <222> (1)..(2)  
 <223> Identity of "Xaa" could not be determined.  
  
 <400> 22  
 Xaa Xaa Leu Ser Cys Ser Lys  
   1                  5  
  
 <210> 23  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
       cleavage peptide  
  
 <400> 23  
 Asp Thr Val Cys Gly Cys Arg  
   1                  5  
  
 <210> 24  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
       cleavage peptide  
  
 <400> 24  
 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys  
   1                  5                  10  
  
 <210> 25  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
       cleavage peptide  
  
 <400> 25  
 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys  
   1                  5                  10  
  
 <210> 26  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>

<221> UNSURE

<222> (6)

<223> Identity of "Xaa" could not be determined.

<220>

<221> UNSURE

<222> (10)..(12)

<223> Identity of "Xaa" could not be determined.

<400> 26

Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys  
1 5 10

<210> 27

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 27

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
1 5 10

<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 28

Leu Val Pro His Leu Gly Asp Arg  
1 5

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 29

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg

1

5

10

15

&lt;210&gt; 30

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

&lt;400&gt; 30

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln

1

5

10

&lt;210&gt; 31

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (9)..(11)

&lt;223&gt; Identity of "Xaa" could not be determined.

&lt;400&gt; 31

Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp

1

5

10

&lt;210&gt; 32

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

&lt;400&gt; 32

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp

1

5

10

15

Thr Val Cys Gly

20

&lt;210&gt; 33

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>  
<221> UNSURE  
<222> (6)  
<223> Identity of "Xaa" could not be determined.

<220>  
<221> UNSURE  
<222> (18)  
<223> Identity of "Xaa" could not be determined.

<400> 33  
Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His Lys  
1 5 10 15

Gly Xaa Tyr

<210> 34  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<220>  
<221> UNSURE  
<222> (16)..(17)  
<223> Identity of "Xaa" could not be determined.

<400> 34  
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Xaa  
1 5 10 15

Xaa Arg

<210> 35  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 35  
Leu Cys Leu Pro Gln Ile Glu Asn  
1 5

<210> 36  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide  
  
 <220>  
 <221> UNSURE  
 <222> (7)  
 <223> Identity of "Xaa" could not be determined.  
  
 <400> 36  
 Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg  
   1                  5                  10  
  
  
 <210> 37  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide  
  
 <400> 37  
 Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn  
   1                  5                  10  
  
  
 <210> 38  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide  
  
 <400> 38  
 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln  
   1                  5                  10  
  
  
 <210> 39  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic  
         cleavage peptide



<400> 39  
Gln Gly Lys Tyr Ile His Pro  
1 5

<210> 40  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 40  
caaggtaa atattcatcc 20

<210> 41  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 41  
cagggtaa gt acatccatcc 20

<210> 42  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 42  
caaggtaa atatacatcc 20

<210> 43  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 43  
caaggcaa atattcatcc 20

<210> 44  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 44  
 cagggcaagt acatccaccc 20  
  
 <210> 45  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 45  
 caaggcaa atatacatcc 20  
  
 <210> 46  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 46  
 caaggaaa atattcatcc 20  
  
 <210> 47  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 47  
 cagggaaagt acatccaccc 20  
  
 <210> 48  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization probe

<400> 48  
 caaggaaaat atatacatcc 20

<210> 49  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization probe

<400> 49  
 caagggaaat atattcatcc 20

<210> 50  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization probe

<400> 50  
 caggggaagt acatccaccc 20

<210> 51  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Hybridization probe

<400> 51  
 caagggaaat atatacatcc 20

<210> 52  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: TNF-BP tryptic cleavage peptide

<400> 52  
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys  
1 5 10

<210> 53  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 53  
Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys  
1 5 10

<210> 54  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 54  
Phe Thr Ala Ser Glu Asn Asn Lys  
1 5

<210> 55  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: TNF-BP tryptic  
cleavage peptide

<400> 55  
Phe Thr Ala Ser Cys Asn Asn Lys  
1 5

<210> 56  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 56

aaatgacgga gactcttggt gttcctaggg

30

<210> 57

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization  
probe

<400> 57

aagtggcgta gtcttttggt gttcctaggg

30

<210> 58

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization  
probe

<400> 58

aaatgtcgga gactcttggt gttcctaggg

30

<210> 59

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization  
probe

<400> 59

aaatgacggt cactcttggt gttcctaggg

30

<210> 60

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization  
probe

<400> 60

aagtggcggt ctcttttggt gttcctaggg

30

<210> 61

<211> 30

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 61  
 aaatgtcggg cactcttggt gttcctaggg 30  
  
  
 <210> 62  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
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       probe  
  
 <400> 62  
 aaatgacgga gaacattggt gttcctaggg 30  
  
  
 <210> 63  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 63  
 aagtggcgta gtactttggt gttcctaggg 30  
  
  
 <210> 64  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization  
       probe  
  
 <400> 64  
 aaatgtcggg gaacattggt gttcctaggg 30  
  
  
 <210> 65  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Hybridization

probe

<400> 65  
aaatgacggt caacattggt gttcctaggg 30

<210> 66  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 66  
aagtggcggt ctactttggt gttcctaggg 30

<210> 67  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Hybridization  
probe

<400> 67  
aaatgtcggt caacattggt gttcctaggg 30

<210> 68  
<211> 158  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(153)

<400> 68  
cag ggg aaa tat att cac cct caa aat aat tcg att tgc tgt acc aag 48  
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys  
1 5 10 15

tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag 96  
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
20 25 30

gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa 144  
Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu  
35 40 45

aac aac aag gatcc 158  
Asn Asn Lys  
50

<210> 69  
<211> 51  
<212> PRT  
<213> Homo sapiens

<400> 69  
Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys  
1 5 10 15  
Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln  
20 25 30  
Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu  
35 40 45  
Asn Asn Lys  
50

<210> 70  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1786

<400> 70  
ggaattcagc ctgaatggcg aatggg

26

<210> 71  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1729

<400> 71  
cctcgagcgt tgctggcggt tttcc

25

<210> 72  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1733

<400> 72



ggtcgacatt gattattgac tag

23

<210> 73

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-1734

<400> 73

ggaattcctt aggaatacag cgg

23

<210> 74

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1751

<400> 74

gtacttgaac tcgttcctg

19

<210> 75

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutagenesis  
primer EBI-1857

<400> 75

ggcaagggca gcagccgg

18

<210> 76

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1823

<400> 76

agcttctgca ggtcgacatc gatggatcgg tacctcgagc ggccgcgaat tct

53

<210> 77

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1829

<400> 77

ctagagaatt cgcggccgct cgaggtaccg gatccatcga tgcgacctg caga 54

<210> 78

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1820

<400> 78

agctctagag attcgcggcc gtcgaggtta ccgcatccat cgatgtcgac ctgcagaagc 60

ttg

63

<210> 79

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Oligonucleotide EBI-1821

<400> 79

ctagcaagct tctgcaggtc gacatcgatg gatccggtac ctcgagcggc cgcgaattct 60

ctag

64

<210> 80

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 80

caggatccga gtctcaaccc tcaac

25

<210> 81

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-1929

<400> 81

gggaattcct tatcaattct caatctgggg taggcacaac ttc

43

<210> 82

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-2452

<400> 82

cacagtcgac ttacatttgc ttctgacaca actgtgttca ctagcaacct caaacagaca 60

ccatgggcct ctccaccgtg c

81

<210> 83

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-1922

<400> 83

gaggctgcaa ttgaagc

17

<210> 84

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-2316

<400> 84

attcgtgcgg cgcctag

17

<210> 85

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
EBI-2467

<400> 85  
gtcggtagca ccaagga

17

<210> 86  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
EBI-1986

<400> 86  
gttttcccag tcacgac

17

<210> 87  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer EBI-2112

<400> 87  
gtccaattat gtcacacc

18